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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
09/219,442	12/23/1998	JING-SHAN HU	PF112P2D1	4797
22195	7590	06/13/2005	EXAMINER	
HUMAN GENOME SCIENCES INC INTELLECTUAL PROPERTY DEPT. 14200 SHADY GROVE ROAD ROCKVILLE, MD 20850			LANDSMAN, ROBERT S	
		ART UNIT	PAPER NUMBER	
		1647		

DATE MAILED: 06/13/2005

Please find below and/or attached an Office communication concerning this application or proceeding.



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APPLICATION NO./ CONTROL NO.	FILING DATE	FIRST NAMED INVENTOR / PATENT IN REEXAMINATION	ATTORNEY DOCKET NO.
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09/219442

12/23/98

Hu et.al.

PF112P2D1

EXAMINER

Landsman

ART UNIT	PAPER
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1647

060805

DATE MAILED:

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Commissioner for Patents

Attached is a PTO Form-892 citing Paulsson et al. A sequence comparison with SEQ ID NO:2 of the present invention is also included. This reference is not considered to have any bearing on patentability of the instant application. It is only submitted to show the closest prior art.


Robert Landsman
Primary Examiner
Art Unit: 1647

SEQ ID NO:2

S08167

Balbiani ring 3 protein - midge (*Chironomus tentans*)

C:Species: Chironomus tentans

C:Date: 30-Sep-1991 #sequence revision 30-Sep-1991 #text change 21-Jul-2000

C:\Accession: S08167

R; Paulsson, G.; Lendahl, U.; Galli, J.; Ericsson, C.; Wieslander, L.
J. Mol. Biol. 211, 331-349, 1990.

A;Title: The balbiani ring 3 gene in *Chironomus tentans* has a diverged repetitive structure split by many introns.

A: Reference number: S08167; MHTD: 001733404

A, Reference Number:
A-Assessments-608163

A;Accession: SU8167
A;Status: not accompanied with specimen label

A;Status: not comparable

A; Molecule type: DNA

A;Residues: 1-1700 <PAU>
A:Cross-references: CRAYE8863 NID: 7057 PDB: 1B7D

A;Cross-ref

C; Genetics:

A;Gene: BR3

A;Map position: 4

Query Match 11.0%; Score 257; DB 2; Length 1700;
Best Local Similarity 22.8%; Pred. No. 4.9e-11;
Matches 89; Conservative 47; Mismatches 145; Indels 110; Gaps
18.

Qy 79 KMYKCQLRK----GGWQHNREQANLNSRTEETIKFAAAHYNTEILKSIDNEWRKTQCMPR 134
 | ||: | | : :||:: :|| | | | : | | |
 Ph 327 KTCGCKCSCPKEMPTCCCGVHIVKIC

Qy 135 EVCIDVGKEFGVATNTFFKPPCVSVYRCGG-----CCNSEGLQCMNTSTS YLSKTLF 186
|| ||: :|| || : :: : : :

Qy 187 EITVPLSQGPKPVTISFANHTSCRCMSKLDV-----YRQVHSIIRRSLPATLPQCQA 238
: | : | : | : | : | : | : | : |

Qy 239 ANKTCPTNYMWNNHICRC---LAQEDFMFSSDAGDDSTDGFHDICG-PNKELD----- 287

Qy 288 -EETCQCVCVRAGLRPASCQPHKELDRNSCQCVCNKLFPSQCQGANREFDENTCQCVCKR- 345

Qy 346 -----TCPQRNQPLNPGKCACECTESPQKCLLKGKKFHH 378

Qy 379 QTCSCYRRPCTNRQKACEPGFSYSEEVCRCV 409

Db 1041 DKCVV---ECAN-VKTCEGPORWCDNQCKCI 106